

## SEQUENCE LISTING

<110> Sims, John E.  
Smith, Dirk E.

<120> IL-1 RECEPTOR ACCESSORY PROTEIN

<130> 3151-A

<140> --to be assigned--  
<141> 2001-10-26

<150> US 60/244,831  
<151> 2000-10-31

<160> 4

<170> PatentIn version 3.1

<210> 1  
<211> 2064  
<212> DNA  
<213> Homo sapiens

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<222> (1)..(2064)  
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<222> (1792)..(1792)  
<223> "n" = a or c. Xaa at amino acid position 598 is Thr or Pro.

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caa agt gat gcc tca gaa cgc tgc gat gac tgg gga cta gac acc atg 96  
Gln Ser Asp Ala Ser Glu Arg Cys Asp Asp Trp Gly Leu Asp Thr Met  
20 25 30

agg caa atc caa gtg ttt gaa gat gag cca gct cgc atc aag tgc cca 144  
Arg Gln Ile Gln Val Phe Glu Asp Glu Pro Ala Arg Ile Lys Cys Pro  
35 40 45

ctc ttt gaa cac ttc ttg aaa ttc aac tac agc aca gcc cat tca gct 192  
Leu Phe Glu His Phe Leu Lys Phe Asn Tyr Ser Thr Ala His Ser Ala  
50 55 60

ggc ctt act ctg atc tgg tat tgg act agg cag gac cgg gac ctt gag 240  
Gly Leu Thr Leu Ile Trp Tyr Trp Thr Arg Gln Asp Arg Asp Leu Glu  
65 70 75 80

gag cca att aac ttc cgc ctc ccc gag aac cgc att agt aag gag aaa 288  
Glu Pro Ile Asn Phe Arg Leu Pro Glu Asn Arg Ile Ser Lys Glu Lys  
85 90 95

gat	gtg	ctg	tgg	ttc	cg	ccc	act	ctc	ctc	aat	gac	act	ggc	aac	tat	336
Asp	Val	Leu	Trp	Phe	Arg	Pro	Thr	Leu	Leu	Asn	Asp	Thr	Gly	Asn	Tyr	
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Thr	Cys	Met	Leu	Arg	Asn	Thr	Thr	Tyr	Cys	Ser	Lys	Val	Ala	Phe	Pro	
115								120				125				
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Leu	Glu	Val	Val	Gln	Lys	Asp	Ser	Cys	Phe	Asn	Ser	Pro	Met	Lys	Leu	
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Pro	Val	His	Lys	Leu	Tyr	Ile	Glu	Tyr	Gly	Ile	Gln	Arg	Ile	Thr	Cys	
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Pro	Asn	Val	Asp	Gly	Tyr	Phe	Pro	Ser	Ser	Val	Lys	Pro	Thr	Ile	Thr	
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Trp	Tyr	Met	Gly	Cys	Tyr	Lys	Ile	Gln	Asn	Phe	Asn	Asn	Val	Ile	Pro	
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gaa	ggt	atg	aac	ttg	agt	ttc	ctc	att	gcc	tta	att	tca	aat	aat	gga	624
Glu	Gly	Met	Asn	Leu	Ser	Phe	Leu	Ile	Ala	Leu	Ile	Ser	Asn	Asn	Gly	
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225							230			235			240			
gtg	ccc	cct	gtg	atc	cat	tca	cct	aat	gat	cat	gtg	gtc	tat	gag	aaa	768
Val	Pro	Pro	Val	Ile	His	Ser	Pro	Asn	Asp	His	Val	Val	Tyr	Glu	Lys	
245							250				255					
gaa	cca	gga	gag	gag	cta	ctc	att	ccc	tgt	acg	gtc	tat	ttt	agt	ttt	816
Glu	Pro	Gly	Glu	Glu	Leu	Leu	Ile	Pro	Cys	Thr	Val	Tyr	Phe	Ser	Phe	
260							265				270					
ctg	atg	gat	tct	cgc	aat	gag	gtt	tgg	acc	att	gat	gga	aaa	aaa	aaa	864
Leu	Met	Asp	Ser	Arg	Asn	Glu	Val	Trp	Trp	Thr	Ile	Asp	Gly	Lys	Lys	
275							280				285					
cct	gat	gac	atc	act	att	gat	gtc	acc	att	aac	gaa	agt	ata	agt	cat	912
Pro	Asp	Asp	Ile	Thr	Ile	Asp	Val	Thr	Ile	Asn	Glu	Ser	Ile	Ser	His	
290							295				300					
agt	aga	aca	gaa	gat	aca	aga	act	cag	att	ttg	agc	atc	aag	aaa	960	
Ser	Arg	Thr	Glu	Asp	Glu	Thr	Arg	Thr	Gln	Ile	Leu	Ser	Ile	Lys	Lys	
305							310			315			320			
gtt	acc	tct	gag	gat	ctc	aag	cgc	agc	tat	gtc	tgt	cat	gct	aga	agt	1008
Val	Thr	Ser	Glu	Asp	Leu	Lys	Arg	Ser	Tyr	Val	Cys	His	Ala	Arg	Ser	
325							330				335					

gcc aaa ggc gaa gtt gcc aaa gca gcc aag gtg aag cag aaa gtg cca Ala Lys Gly Val Ala Lys Ala Ala Lys Val Lys Gln Lys Val Pro 340 345 350	1056
gct cca aga tac aca gtg gaa ctg gct tgt ggt ttt gga gcc aca gtc Ala Pro Arg Tyr Thr Val Glu Leu Ala Cys Gly Phe Gly Ala Thr Val 355 360 365	1104
ctg cta gtg gtg att ctc att gtt gtt tac cat gtt tac tgg cta gag Leu Leu Val Val Ile Leu Ile Val Val Tyr His Val Tyr Trp Leu Glu 370 375 380	1152
atg gtc cta ttt tac cgg gct cat ttt gga aca gat gaa acc att tta Met Val Leu Phe Tyr Arg Ala His Phe Gly Thr Asp Glu Thr Ile Leu 385 390 395 400	1200
gat gga aaa gag tat gat att tat gta tcc tat gca agg aat gcg gaa Asp Gly Lys Glu Tyr Asp Ile Tyr Val Ser Tyr Ala Arg Asn Ala Glu 405 410 415	1248
gaa gaa gaa ttt gta tta ctg acc ctc cgt gga gtt ttg gag aat gaa Glu Glu Glu Phe Val Leu Leu Thr Leu Arg Gly Val Leu Glu Asn Glu 420 425 430	1296
ttt gga tac aag ctg tgc atc ttt gac cga gac agt ctg cct ggg gga Phe Gly Tyr Lys Leu Cys Ile Phe Asp Arg Asp Ser Leu Pro Gly Gly 435 440 445	1344
aat aca gtg gaa gca gtt ttt gat ttc att cag aga agc aga agg atg Asn Thr Val Glu Ala Val Phe Asp Phe Ile Gln Arg Ser Arg Arg Met 450 455 460	1392
att gtt gtt ctg agc cct gac tat gtg aca gaa aag agc atc agc atg Ile Val Val Leu Ser Pro Asp Tyr Val Thr Glu Lys Ser Ile Ser Met 465 470 475 480	1440
ctg gag ttt aaa ctg ggt gtc atg tgc cag aac tcc att gcc acc aag Leu Glu Phe Lys Leu Gly Val Met Cys Gln Asn Ser Ile Ala Thr Lys 485 490 495	1488
ctc att gtg gtt gag tac cgt ccc ctt gag cac ccg cac cca ggc att Leu Ile Val Val Glu Tyr Arg Pro Leu Glu His Pro His Pro Gly Ile 500 505 510	1536
ctt cag ctc aaa gag tct gtg tct ttt gtg agc tgg aag gga gaa aag Leu Gln Leu Lys Glu Ser Val Ser Phe Val Ser Trp Lys Gly Glu Lys 515 520 525	1584
tcc aaa cat tct ggc tct aaa ttc tgg aaa gct ttg cgg ttg gct ctt Ser Lys His Ser Gly Ser Lys Phe Trp Lys Ala Leu Arg Leu Ala Leu 530 535 540	1632
ccc ctg aga agt ctg agt ggc agt tct ggc tgg aat gag agc tgc tct Pro Leu Arg Ser Leu Ser Ala Ser Ser Gly Trp Asn Glu Ser Cys Ser 545 550 555 560	1680
tcc cag tct gac atc agt ctg gat cac gtt caa agg agg aga agt cgt Ser Gln Ser Asp Ile Ser Leu Asp His Val Gln Arg Arg Arg Ser Arg 565 570 575	1728

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 Leu Lys Glu Pro Pro Glu Leu Gln Ser Ser Glu Arg Ala Ala Gly Ser  
 580 585 590

cct cca gcc cca ggc nca atg tcc aag cac cga ggg aag tcc tcc gcc 1824  
 Pro Pro Ala Pro Gly Xaa Met Ser Lys His Arg Gly Lys Ser Ser Ala  
 595 600 605

acc tgc cgc tgt tgt gtc acc tac tgt gaa gga gag aat cac ctt agg 1872  
 Thr Cys Arg Cys Cys Val Thr Tyr Cys Glu Gly Glu Asn His Leu Arg  
 610 615 620

aac aag agc cgg gca gag att cat aac cag ccc cag tgg gag aca cac 1920  
 Asn Lys Ser Arg Ala Glu Ile His Asn Gln Pro Gln Trp Glu Thr His  
 625 630 635 640

ctc tgt aag cct gtt ccc caa gag tca gaa act caa tgg ata caa aat 1968  
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 645 650 655

ggc acc aga ttg gaa ccc cct gct ccc cag atc tca gcc ctt gct ctt 2016  
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 660 665 670

cat cat ttc acg gac tta tcc aat aac aac gac ttt tat atc cta taa 2064  
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 675 680 685

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Arg Gln Ile Gln Val Phe Glu Asp Glu Pro Ala Arg Ile Lys Cys Pro  
 35 40 45

Leu Phe Glu His Phe Leu Lys Phe Asn Tyr Ser Thr Ala His Ser Ala  
 50 55 60

Gly Leu Thr Leu Ile Trp Tyr Trp Thr Arg Gln Asp Arg Asp Leu Glu  
 65 70 75 80

Glu Pro Ile Asn Phe Arg Leu Pro Glu Asn Arg Ile Ser Lys Glu Lys  
85 90 95

Asp Val Leu Trp Phe Arg Pro Thr Leu Leu Asn Asp Thr Gly Asn Tyr  
100 105 110

Thr Cys Met Leu Arg Asn Thr Thr Tyr Cys Ser Lys Val Ala Phe Pro  
115 120 125

Leu Glu Val Val Gln Lys Asp Ser Cys Phe Asn Ser Pro Met Lys Leu  
130 135 140

Pro Val His Lys Leu Tyr Ile Glu Tyr Gly Ile Gln Arg Ile Thr Cys  
145 150 155 160

Pro Asn Val Asp Gly Tyr Phe Pro Ser Ser Val Lys Pro Thr Ile Thr  
165 170 175

Trp Tyr Met Gly Cys Tyr Lys Ile Gln Asn Phe Asn Asn Val Ile Pro  
180 185 190

Glu Gly Met Asn Leu Ser Phe Leu Ile Ala Leu Ile Ser Asn Asn Gly  
195 200 205

Asn Tyr Thr Cys Val Val Thr Tyr Pro Glu Asn Gly Arg Thr Phe His  
210 215 220

Leu Thr Arg Thr Leu Thr Val Lys Val Val Gly Ser Pro Lys Asn Ala  
225 230 235 240

Val Pro Pro Val Ile His Ser Pro Asn Asp His Val Val Tyr Glu Lys  
245 250 255

Glu Pro Gly Glu Glu Leu Leu Ile Pro Cys Thr Val Tyr Phe Ser Phe  
260 265 270

Leu Met Asp Ser Arg Asn Glu Val Trp Trp Thr Ile Asp Gly Lys Lys  
275 280 285

Pro Asp Asp Ile Thr Ile Asp Val Thr Ile Asn Glu Ser Ile Ser His  
290 295 300

Ser Arg Thr Glu Asp Glu Thr Arg Thr Gln Ile Leu Ser Ile Lys Lys  
305 310 315 320

Val Thr Ser Glu Asp Leu Lys Arg Ser Tyr Val Cys His Ala Arg Ser  
325 330 335

Ala Lys Gly Glu Val Ala Lys Ala Ala Lys Val Lys Gln Lys Val Pro  
340 345 350

Ala Pro Arg Tyr Thr Val Glu Leu Ala Cys Gly Phe Gly Ala Thr Val  
355 360 365

Leu Leu Val Val Ile Leu Ile Val Val Tyr His Val Tyr Trp Leu Glu  
370 375 380

Met Val Leu Phe Tyr Arg Ala His Phe Gly Thr Asp Glu Thr Ile Leu  
385 390 395 400

Asp Gly Lys Glu Tyr Asp Ile Tyr Val Ser Tyr Ala Arg Asn Ala Glu  
405 410 415

Glu Glu Glu Phe Val Leu Leu Thr Leu Arg Gly Val Leu Glu Asn Glu  
420 425 430

Phe Gly Tyr Lys Leu Cys Ile Phe Asp Arg Asp Ser Leu Pro Gly Gly  
435 440 445

Asn Thr Val Glu Ala Val Phe Asp Phe Ile Gln Arg Ser Arg Arg Met  
450 455 460

Ile Val Val Leu Ser Pro Asp Tyr Val Thr Glu Lys Ser Ile Ser Met  
465 470 475 480

Leu Glu Phe Lys Leu Gly Val Met Cys Gln Asn Ser Ile Ala Thr Lys  
485 490 495

Leu Ile Val Val Glu Tyr Arg Pro Leu Glu His Pro His Pro Gly Ile  
500 505 510

Leu Gln Leu Lys Glu Ser Val Ser Phe Val Ser Trp Lys Gly Glu Lys  
515 520 525

Ser Lys His Ser Gly Ser Lys Phe Trp Lys Ala Leu Arg Leu Ala Leu  
530 535 540

Pro Leu Arg Ser Leu Ser Ala Ser Ser Gly Trp Asn Glu Ser Cys Ser  
545 550 555 560

Ser Gln Ser Asp Ile Ser Leu Asp His Val Gln Arg Arg Arg Ser Arg  
 565 570 575

Leu Lys Glu Pro Pro Glu Leu Gln Ser Ser Glu Arg Ala Ala Gly Ser  
 580 585 590

Pro Pro Ala Pro Gly Xaa Met Ser Lys His Arg Gly Lys Ser Ser Ala  
 595 600 605

Thr Cys Arg Cys Cys Val Thr Tyr Cys Glu Gly Glu Asn His Leu Arg  
 610 615 620

Asn Lys Ser Arg Ala Glu Ile His Asn Gln Pro Gln Trp Glu Thr His  
 625 630 635 640

Leu Cys Lys Pro Val Pro Gln Glu Ser Glu Thr Gln Trp Ile Gln Asn  
 645 650 655

Gly Thr Arg Leu Glu Pro Pro Ala Pro Gln Ile Ser Ala Leu Ala Leu  
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His His Phe Thr Asp Leu Ser Asn Asn Asn Asp Phe Tyr Ile Leu  
 675 680 685

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 1 5 10 15

cag agt cat gct tcg gag cgc tgt gat gac tgg gga cta gat acc atg 96  
 Gln Ser His Ala Ser Glu Arg Cys Asp Asp Trp Gly Leu Asp Thr Met  
 20 25 30

cga caa atc caa gtg ttt gaa gat gag ccg gct cga atc aag tgc ccc 144  
 Arg Gln Ile Gln Val Phe Glu Asp Glu Pro Ala Arg Ile Lys Cys Pro  
 35 40 45

ctc ttt gaa cac ttc ctg aag tac aac tac agc act gcc cat tcc tct 192  
 Leu Phe Glu His Phe Leu Lys Tyr Asn Tyr Ser Thr Ala His Ser Ser  
 50 55 60

ggc ctt acc ctg atc tgg tac tgg acc agg caa gac gac ctg gag	240
Gly Leu Thr Leu Ile Trp Tyr Trp Thr Arg Gln Asp Arg Asp Leu Glu	
65 70 75 80	
gag ccc att aac ttc cgc ctc cca gag aat cgc atc agt aag gag aaa	288
Glu Pro Ile Asn Phe Arg Leu Pro Glu Asn Arg Ile Ser Lys Glu Lys	
85 90 95	
gat gtg ctc tgg ttc cgg ccc acc ctc ctc aat gac acg ggc aat tac	336
Asp Val Leu Trp Phe Arg Pro Thr Leu Leu Asn Asp Thr Gly Asn Tyr	
100 105 110	
acc tgc atg ttg agg aac aca act tac tgc agc aaa gtt gca ttt ccc	384
Thr Cys Met Leu Arg Asn Thr Thr Tyr Cys Ser Lys Val Ala Phe Pro	
115 120 125	
ctg gaa gtt gtt cag aag gac agc tgt ttc aat tct gcc atg aga ttc	432
Leu Glu Val Val Gln Lys Asp Ser Cys Phe Asn Ser Ala Met Arg Phe	
130 135 140	
cca gtg cac aag atg tat att gaa cat ggc att cat aag atc aca tgt	480
Pro Val His Lys Met Tyr Ile Glu His Gly Ile His Lys Ile Thr Cys	
145 150 155 160	
cca aat gta gac gga tac ttt cct tcc agt gtc aaa cca tcg gtc act	528
Pro Asn Val Asp Gly Tyr Phe Pro Ser Ser Val Lys Pro Ser Val Thr	
165 170 175	
tgg tat aag ggt tgt act gaa ata gtg gac ttt cat aat gta cta ccc	576
Trp Tyr Lys Gly Cys Thr Glu Ile Val Asp Phe His Asn Val Leu Pro	
180 185 190	
gag ggc atg aac ttg agc ttt atc ccc ttg gtt tca aat aac gga	624
Glu Gly Met Asn Leu Ser Phe Phe Ile Pro Leu Val Ser Asn Asn Gly	
195 200 205	
aat tac aca tgt gtg gtt aca tat cct gaa aac gga cgt ctc ttt cac	672
Asn Tyr Thr Cys Val Val Thr Tyr Pro Glu Asn Gly Arg Leu Phe His	
210 215 220	
ctc acc agg act gtg act gta aag gtg gtg ggc tca cca aag gat gca	720
Leu Thr Arg Thr Val Thr Val Lys Val Val Gly Ser Pro Lys Asp Ala	
225 230 235 240	
ttg cca ccc cag atc tat tct cca aat gac cgt gtt gtc tat gag aaa	768
Leu Pro Pro Gln Ile Tyr Ser Pro Asn Asp Arg Val Val Tyr Glu Lys	
245 250 255	
gaa cca gga gag gaa ctg gtt att ccc tgc aaa gtc tat ttc agt ttc	816
Glu Pro Gly Glu Glu Leu Val Ile Pro Cys Lys Val Tyr Phe Ser Phe	
260 265 270	
att atg gac tcc cac aat gag gtc tgg tgg acc att gat gga aag aag	864
Ile Met Asp Ser His Asn Glu Val Trp Trp Thr Ile Asp Gly Lys Lys	
275 280 285	
cct gat gac gtc aca gtc gac atc act att aat gaa agt gta agt tat	912
Pro Asp Asp Val Thr Val Asp Ile Thr Ile Asn Glu Ser Val Ser Tyr	
290 295 300	

tct tca acg gaa gat gaa aca agg act cag att ttg agc atc aag aaa Ser Ser Thr Glu Asp Glu Thr Arg Thr Gln Ile Leu Ser Ile Lys Lys 305 310 315 320	960
gtc acc ccg gag gat ctc agg cgc aac tat gtc tgt cat gct cga aat Val Thr Pro Glu Asp Leu Arg Arg Asn Tyr Val Cys His Ala Arg Asn 325 330 335	1008
acc aaa ggg gaa gct gag cag gct gcc aag gtg aaa cag aaa gtc ata Thr Lys Gly Glu Ala Glu Gln Ala Ala Lys Val Lys Gln Lys Val Ile 340 345 350	1056
cca cca agg tac aca gta gaa ctc gcc tgt ggt ttt gga gcc acg gtc Pro Pro Arg Tyr Thr Val Glu Leu Ala Cys Gly Phe Gly Ala Thr Val 355 360 365	1104
ttt ctg gta gtg gtt ctc att gtg gtt tac cat gtt tac tgg ctg gag Phe Leu Val Val Val Leu Ile Val Val Tyr His Val Tyr Trp Leu Glu 370 375 380	1152
atg gtc ctc ttt tac cga gct cac ttt gga aca gat gaa aca att ctt Met Val Leu Phe Tyr Arg Ala His Phe Gly Thr Asp Glu Thr Ile Leu 385 390 395 400	1200
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gaa gag gaa ttt gtg ctg ctg acg ctg cgt gga gtt ttg gag aat gag Glu Glu Glu Phe Val Leu Leu Thr Leu Arg Gly Val Leu Glu Asn Glu 420 425 430	1296
ttt gga tac aag ctg tgc atc ttc gac aga gac agc ctg cct ggg gga Phe Gly Tyr Lys Leu Cys Ile Phe Asp Arg Asp Ser Leu Pro Gly Gly 435 440 445	1344
aat acc gtg gaa gca gtt ttt gat ttc att cag agg agc cga agg atg Asn Thr Val Glu Ala Val Phe Asp Phe Ile Gln Arg Ser Arg Arg Met 450 455 460	1392
att gtt gtc ctg agc cct gac tat gtg aca gaa aag agc atc agc atg Ile Val Val Leu Ser Pro Asp Tyr Val Thr Glu Lys Ser Ile Ser Met 465 470 475 480	1440
ctg gag ttt aag ctg ggt gtc atg tgc cag aac tcc att gcc act aag Leu Glu Phe Lys Leu Gly Val Met Cys Gln Asn Ser Ile Ala Thr Lys 485 490 495	1488
ctc att gtg gtg gag tac cgt ccg ctt gag caa ccc cat cca ggc atc Leu Ile Val Val Glu Tyr Arg Pro Leu Glu Gln Pro His Pro Gly Ile 500 505 510	1536
atg cag ctg aag gag tct gtg tct ttt gta agc tgg aag gga gaa aag Met Gln Leu Lys Glu Ser Val Ser Phe Val Ser Trp Lys Gly Glu Lys 515 520 525	1584
tcc aaa cat tct ggc tcc aag ttc tgg aag gcc ttg cgt ttg gct ctt Ser Lys His Ser Gly Ser Lys Phe Trp Lys Ala Leu Arg Leu Ala Leu 530 535 540	1632

ccc ctg aga agt ctg agc gcc agc tcc ggc tgg aat gag agc tgt tct 1680  
 Pro Leu Arg Ser Leu Ser Ala Ser Ser Gly Trp Asn Glu Ser Cys Ser  
 545 550 555 560

tct cag tct gac atc agt ctg gat cat gtt cag agg aga agt cgt ttg 1728  
 Ser Gln Ser Asp Ile Ser Leu Asp His Val Gln Arg Arg Ser Arg Leu  
 565 570 575

aaa gag ccc cca gaa ctc cga agc tca gag agg gtg tct gga gca gag 1776  
 Lys Glu Pro Pro Glu Leu Arg Ser Ser Glu Arg Val Ser Gly Ala Glu  
 580 585 590

cca gcc ccg ggc acg atg tcc aag cac cga ggg aaa ccc tca gca gcc 1824  
 Pro Ala Pro Gly Thr Met Ser Lys His Arg Gly Lys Pro Ser Ala Ala  
 595 600 605

tgt cgc tgc tgt gtc acc tac tgt gaa gga gaa agt cac ctc agg agc 1872  
 Cys Arg Cys Cys Val Thr Tyr Cys Glu Gly Glu Ser His Leu Arg Ser  
 610 615 620

aag agc cgg gca gag atg cac acg cat ccc cag tgg gaa aca cac ctc 1920  
 Lys Ser Arg Ala Glu Met His Thr His Pro Gln Trp Glu Thr His Leu  
 625 630 635 640

tgt aag cct ctc caa gag tct gaa agt cag tgg ata caa aat ggc 1968  
 Cys Lys Pro Pro Leu Gln Glu Ser Glu Ser Gln Trp Ile Gln Asn Gly  
 645 650 655

acc cga ccc gaa ccc gct ccc cag atc tca gct ctt gca ctc cgc cac 2016  
 Thr Arg Pro Glu Pro Ala Pro Gln Ile Ser Ala Leu Ala Leu Arg His  
 660 665 670

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 675 680 685

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<400> 4

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Arg Gln Ile Gln Val Phe Glu Asp Glu Pro Ala Arg Ile Lys Cys Pro  
 35 40 45

Leu Phe Glu His Phe Leu Lys Tyr Asn Tyr Ser Thr Ala His Ser Ser  
 50 55 60

Gly Leu Thr Leu Ile Trp Tyr Trp Thr Arg Gln Asp Arg Asp Leu Glu  
65 70 75 80

Glu Pro Ile Asn Phe Arg Leu Pro Glu Asn Arg Ile Ser Lys Glu Lys  
85 90 95

Asp Val Leu Trp Phe Arg Pro Thr Leu Leu Asn Asp Thr Gly Asn Tyr  
100 105 110

Thr Cys Met Leu Arg Asn Thr Thr Tyr Cys Ser Lys Val Ala Phe Pro  
115 120 125

Leu Glu Val Val Gln Lys Asp Ser Cys Phe Asn Ser Ala Met Arg Phe  
130 135 140

Pro Val His Lys Met Tyr Ile Glu His Gly Ile His Lys Ile Thr Cys  
145 150 155 160

Pro Asn Val Asp Gly Tyr Phe Pro Ser Ser Val Lys Pro Ser Val Thr  
165 170 175

Trp Tyr Lys Gly Cys Thr Glu Ile Val Asp Phe His Asn Val Leu Pro  
180 185 190

Glu Gly Met Asn Leu Ser Phe Phe Ile Pro Leu Val Ser Asn Asn Gly  
195 200 205

Asn Tyr Thr Cys Val Val Thr Tyr Pro Glu Asn Gly Arg Leu Phe His  
210 215 220

Leu Thr Arg Thr Val Thr Val Lys Val Val Gly Ser Pro Lys Asp Ala  
225 230 235 240

Leu Pro Pro Gln Ile Tyr Ser Pro Asn Asp Arg Val Val Tyr Glu Lys  
245 250 255

Glu Pro Gly Glu Glu Leu Val Ile Pro Cys Lys Val Tyr Phe Ser Phe  
260 265 270

Ile Met Asp Ser His Asn Glu Val Trp Trp Thr Ile Asp Gly Lys Lys  
275 280 285

Pro Asp Asp Val Thr Val Asp Ile Thr Ile Asn Glu Ser Val Ser Tyr  
290 295 300

Ser Ser Thr Glu Asp Glu Thr Arg Thr Gln Ile Leu Ser Ile Lys Lys  
305 310 315 320

Val Thr Pro Glu Asp Leu Arg Arg Asn Tyr Val Cys His Ala Arg Asn  
325 330 335

Thr Lys Gly Glu Ala Glu Gln Ala Ala Lys Val Lys Gln Lys Val Ile  
340 345 350

Pro Pro Arg Tyr Thr Val Glu Leu Ala Cys Gly Phe Gly Ala Thr Val  
355 360 365

Phe Leu Val Val Val Leu Ile Val Val Tyr His Val Tyr Trp Leu Glu  
370 375 380

Met Val Leu Phe Tyr Arg Ala His Phe Gly Thr Asp Glu Thr Ile Leu  
385 390 395 400

Asp Gly Lys Glu Tyr Asp Ile Tyr Val Ser Tyr Ala Arg Asn Val Glu  
405 410 415

Glu Glu Glu Phe Val Leu Leu Thr Leu Arg Gly Val Leu Glu Asn Glu  
420 425 430

Phe Gly Tyr Lys Leu Cys Ile Phe Asp Arg Asp Ser Leu Pro Gly Gly  
435 440 445

Asn Thr Val Glu Ala Val Phe Asp Phe Ile Gln Arg Ser Arg Arg Met  
450 455 460

Ile Val Val Leu Ser Pro Asp Tyr Val Thr Glu Lys Ser Ile Ser Met  
465 470 475 480

Leu Glu Phe Lys Leu Gly Val Met Cys Gln Asn Ser Ile Ala Thr Lys  
485 490 495

Leu Ile Val Val Glu Tyr Arg Pro Leu Glu Gln Pro His Pro Gly Ile  
500 505 510

Met Gln Leu Lys Glu Ser Val Ser Phe Val Ser Trp Lys Gly Glu Lys  
515 520 525

Ser Lys His Ser Gly Ser Lys Phe Trp Lys Ala Leu Arg Leu Ala Leu  
530 535 540

Pro Leu Arg Ser Leu Ser Ala Ser Ser Gly Trp Asn Glu Ser Cys Ser  
545 550 555 560

Ser Gln Ser Asp Ile Ser Leu Asp His Val Gln Arg Arg Ser Arg Leu  
565 570 575

Lys Glu Pro Pro Glu Leu Arg Ser Ser Glu Arg Val Ser Gly Ala Glu  
580 585 590

Pro Ala Pro Gly Thr Met Ser Lys His Arg Gly Lys Pro Ser Ala Ala  
595 600 605

Cys Arg Cys Cys Val Thr Tyr Cys Glu Gly Glu Ser His Leu Arg Ser  
610 615 620

Lys Ser Arg Ala Glu Met His Thr His Pro Gln Trp Glu Thr His Leu  
625 630 635 640

Cys Lys Pro Pro Leu Gln Glu Ser Glu Ser Gln Trp Ile Gln Asn Gly  
645 650 655

Thr Arg Pro Glu Pro Ala Pro Gln Ile Ser Ala Leu Ala Leu Arg His  
660 665 670

Phe Thr Asp Leu Ser Asn Asn Asn Asp Phe Tyr Ile Leu  
675 680 685